

OIPE

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 PATENT APPLICATION: US/09/866,020

DATE: 06/21/2001
 TIME: 16:20:06

#2

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3 <110> APPLICANT: DWORETZKY, STEVEN I
 4 RAMANATHAN, CHANDRA S
 5 TROJNACKI, JOANNE T
 6 BOISSARD, CHRISTOPHER G
 7 GRIBKOFF, VALENTIN K
 9 <120> TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
 10 THEREOF
 12 <130> FILE REFERENCE: 3053-4091US1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/866,020
 15 <141> CURRENT FILING DATE: 2001-05-24
 17 <150> PRIOR APPLICATION NUMBER: 60/207,389
 18 <151> PRIOR FILING DATE: 2000-05-26
 20 <160> NUMBER OF SEQ ID NOS: 31
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2694
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
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 32 agggagagcc gccggggcaa gcagggggcc cggatgagcc tgctggggaa gccgctctct 180
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60 gcctcagccc tcgctttggc ttcatccag atccacactt ttgaatgtga acagacatct 1860
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62 ttatccagat caactagtgc caacatctcg agaggcctgc agttcattct gacgccaaat 1980
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77 <210> SEQ ID NO: 2

78 <211> LENGTH: 897

79 <212> TYPE: PRT

80 <213> ORGANISM: Homo sapiens

82 <400> SEQUENCE: 2

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87             20             25             30
89 Leu Gly Gly Gly Gly Gly Gly Leu Arg Glu Ser Arg Arg Gly Lys Gln
90             35             40             45
92 Gly Ala Arg Met Ser Leu Leu Gly Lys Pro Leu Ser Tyr Thr Ser Ser
93             50             55             60
95 Gln Ser Cys Arg Arg Asn Val Lys Tyr Arg Arg Val Gln Asn Tyr Leu
96   65             70             75             80
98 Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His Ala
99             85             90             95
101 Phe Val Phe Leu Leu Val Phe Gly Cys Leu Ile Leu Ser Val Phe Ser
102             100            105            110
104 Thr Ile Pro Glu His Thr Lys Leu Ala Ser Ser Cys Leu Leu Ile Leu
105             115            120            125
107 Glu Phe Val Met Ile Val Val Phe Gly Leu Glu Phe Ile Ile Arg Ile
108             130            135            140
110 Trp Ser Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Leu
111   145            150            155            160
113 Arg Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Thr Ile Val Leu Ile
114             165            170            175
116 Ala Ser Ile Ala Val Val Ser Ala Lys Thr Gln Gly Asn Ile Phe Ala
117             180            185            190
119 Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met Val
120             195            200            205
122 Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val

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123      210      215      220
125 Tyr Ala His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu
126 225      230      235      240
128 Val Leu Ile Phe Ser Ser Phe Leu Val Tyr Leu Val Glu Lys Asp Ala
129      245      250      255
131 Asn Lys Glu Phe Ser Thr Tyr Ala Asp Ala Leu Trp Trp Gly Thr Ile
132      260      265      270
134 Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Thr Pro Leu Thr Trp Leu
135      275      280      285
137 Gly Arg Leu Leu Ser Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe
138      290      295      300
140 Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln
141 305      310      315      320
143 Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala Ala
144      325      330      335
146 Asn Leu Ile Gln Cys Val Trp Arg Ser Tyr Ala Ala Asp Glu Lys Ser
147      340      345      350
149 Val Ser Ile Ala Thr Trp Lys Pro His Leu Lys Ala Leu His Thr Cys
150      355      360      365
152 Ser Pro Thr Lys Lys Glu Gln Gly Glu Ala Ser Ser Ser Gln Lys Leu
153      370      375      380
155 Ser Phe Lys Glu Arg Val Arg Met Ala Ser Pro Arg Gly Gln Ser Ile
156 385      390      395      400
158 Lys Ser Arg Gln Ala Ser Val Gly Asp Arg Arg Ser Pro Ser Thr Asp
159      405      410      415
161 Ile Thr Ala Glu Gly Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe
162      420      425      430
164 Asn Asp Arg Thr Arg Phe Arg Pro Ser Leu Arg Leu Lys Ser Ser Gln
165      435      440      445
167 Pro Lys Pro Val Ile Asp Ala Asp Thr Ala Leu Gly Thr Asp Asp Val
168      450      455      460
170 Tyr Asp Glu Lys Gly Cys Gln Cys Asp Val Ser Val Glu Asp Leu Thr
171 465      470      475      480
173 Pro Pro Leu Lys Thr Val Ile Arg Ala Ile Arg Ile Met Lys Phe His
174      485      490      495
176 Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
177      500      505      510
179 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Cys Arg
180      515      520      525
182 Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Leu Gly Lys Gly Gln
183      530      535      540
185 Ile Thr Ser Asp Lys Lys Ser Arg Glu Lys Ile Thr Ala Glu His Glu
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188 Thr Thr Asp Asp Leu Ser Met Leu Gly Arg Val Val Lys Val Glu Lys
189      565      570      575
191 Gln Val Gln Ser Ile Glu Ser Lys Leu Asp Cys Leu Leu Asp Ile Tyr
192      580      585      590
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197 Phe Gln Ile Pro Pro Phe Glu Cys Glu Gln Thr Ser Asp Tyr Gln Ser
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201 625                      630                      635                      640
203 Leu Ser Arg Ser Thr Ser Ala Asn Ile Ser Arg Gly Leu Gln Phe Ile
204                      645                      650                      655
206 Leu Thr Pro Asn Glu Phe Ser Ala Gln Thr Phe Tyr Ala Leu Ser Pro
207                      660                      665                      670
209 Thr Met His Ser Gln Ala Thr Gln Val Pro Ile Ser Gln Ser Asp Gly
210                      675                      680                      685
212 Ser Ala Val Ala Ala Thr Asn Thr Ile Ala Asn Gln Ile Asn Thr Ala
213      690                      695                      700
215 Pro Lys Pro Ala Ala Pro Thr Thr Leu Gln Ile Pro Pro Pro Leu Pro
216 705                      710                      715                      720
218 Ala Ile Lys His Leu Pro Arg Pro Glu Thr Leu His Pro Asn Pro Ala
219                      725                      730                      735
221 Gly Leu Gln Glu Ser Ile Ser Asp Val Thr Thr Cys Leu Val Ala Ser
222                      740                      745                      750
224 Lys Glu Asn Val Gln Val Ala Gln Ser Asn Leu Thr Lys Asp Arg Ser
225                      755                      760                      765
227 Met Arg Lys Ser Phe Asp Met Gly Gly Glu Thr Leu Leu Ser Val Cys
228      770                      775                      780
230 Pro Met Val Pro Lys Asp Leu Gly Lys Ser Leu Ser Val Gln Asn Leu
231 785                      790                      795                      800
233 Ile Arg Ser Thr Glu Glu Leu Asn Ile Gln Leu Ser Gly Ser Glu Ser
234                      805                      810                      815
236 Ser Gly Ser Arg Gly Ser Gln Asp Phe Tyr Pro Lys Trp Arg Glu Ser
237                      820                      825                      830
239 Lys Leu Phe Ile Thr Asp Glu Glu Val Gly Pro Glu Glu Thr Glu Thr
240                      835                      840                      845
242 Asp Thr Phe Asp Ala Ala Pro Gln Pro Ala Arg Glu Ala Ala Phe Ala
243      850                      855                      860
245 Ser Asp Ser Leu Arg Thr Gly Arg Ser Arg Ser Ser Gln Ser Ile Cys
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251 Lys

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256 <211> LENGTH: 21

257 <212> TYPE: DNA

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262 <222> LOCATION: (1)..(21)

264 <220> FEATURE:

265 <221> NAME/KEY: CDS

266 <222> LOCATION: (1)..(21)

268 <400> SEQUENCE: 3

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21

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270 Trp Gly Gln Trp Thr Leu Arg

271 1 5

274 <210> SEQ ID NO: 4

275 <211> LENGTH: 7

276 <212> TYPE: PRT

277 <213> ORGANISM: Homo sapiens

279 <400> SEQUENCE: 4

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281 1 5

285 <210> SEQ ID NO: 5

286 <211> LENGTH: 1090

287 <212> TYPE: DNA

288 <213> ORGANISM: Homo sapiens

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294 <400> SEQUENCE: 5

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329 <210> SEQ ID NO: 7

330 <211> LENGTH: 23

331 <212> TYPE: PRT

332 <213> ORGANISM: Homo sapiens

334 <400> SEQUENCE: 7

VERIFICATION SUMMARY

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